



#7/13

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Clinton, Gail and Doherty, Joni Kristin
- (ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DAVIS WRIGHT TREMAINE
 - (B) STREET: 1501 Fourth Avenue, 2600 Century Square
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: PC compatible
 - (C) OPERATING SYSTEM: Windows95
 - (D) SOFTWARE: Word
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: to be assigned
 - (B) FILING DATE: 19 January 1999
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Oster, Jeffrey B.
 - (B) REGISTRATION NUMBER: 32,585
 - (C) REFERENCE/DOCKET NUMBER: OHSU-1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 206 628 7711
 - (B) TELEFAX: 206 628 7699

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: HER-2 ECD antagonist
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly	Thr	His	Ser	Leu	Leu	Pro	Arg	Pro	Ala	Ala	Val	Pro	Val	Pro	Leu
				5					10					15	
Arg	Met	Gln	Pro	Gly	Pro	Ala	His	Pro	Val	Leu	Ser	Phe	Leu	Arg	Pro
			20					25					30		
Ser	Trp	Asp	Leu	Val	Ser	Ala	Phe	Tyr	Ser	Leu	Pro	Leu	Ala	Pro	Leu
		35					40					45			
Ser	Pro	Thr	Ser	Val	Pro	Ile	Ser	Pro	Val	Ser	Val	Gly	Arg	Gly	Pro
	50					55					60				
Asp	Pro	Asp	Ala	His	Val	Ala	Val	Asn	Leu	Ser	Arg	Tyr	Glu	Gly	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu
				5					10					15	
Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Cys	Lys
			20					25					30		
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His
		35					40					45			
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr
	50					55					60				
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val
	65				70					75					
Gln	Gly	Tyr	Val	Leu	Cys	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu
80				85					90					95	
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr
			100					105					110		
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Agn	Agn	Thr	Thr	Pro
		115					120						125		
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser
	130					135						140			
Leu	Thr	Glu	Cys	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln
	145				150					155					
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn
160				165					170					175	
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys
			180					185					190		
His	Pro	Cys	Ser	Pro	Cys	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser
		195					200						205		

Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys
	210						215					220			
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys
	225					230					235				
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu
240					245					250					255
His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val
			260						265					270	
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Cys	Pro	Asn	Pro	Glu	Gly	Arg
		275						280					285		
Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Lys	Leu
	290						295				300				
Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Leu	His	Asn	Gln
	305					310					315				
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys
320				325						330					335
Pro	Cys	Ala	Arg	Val	Gly	Thr	His	Ser	Leu	Leu	Pro	Arg	Pro	Ala	Ala
			340						345					350	
Val	Pro	Val	Pro	Leu	Arg	Met	Gln	Pro	Gly	Pro	Ala	His	Pro	Val	Leu
		355					360					365			
Ser	Phe	Leu	Arg	Pro	Ser	Trp	Asp	Leu	Val	Ser	Ala	Phe	Tyr	Ser	Leu
	370						375				380				
Pro	Leu	Ala	Pro	Leu	Asp	Pro	Thr	Ser	Val	Pro	Ile	Ser	Pro	Val	Ser
	385				390						395				
Val	Gly	Arg	Gly	Pro	Asp	Pro	Asp	Ala	His	Val	Ala	Val	Asn	Leu	Ser
400				405						410					415
Arg	Tyr	Glu	Gly												

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGAGCACCAT GGAGCTGGC 19

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCCGGCAGAA ATGCCAGGCT CC 22

- (2) INFORMATION FOR SEQ ID NO:5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: oligonucleotide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACACAGCGG TGTGAGAAGT GC 22

- (2) INFORMATION FOR SEQ ID NO:6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: oligonucleotide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATACCGGGAC AGGTCAACAG C 21

- (2) INFORMATION FOR SEQ ID NO:7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: oligonucleotide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTGGGTACC CACTCACTGC 20

- (2) INFORMATION FOR SEQ ID NO:8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: oligonucleotide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCACACTGG CACGTCCAGA CC 22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCACGGATCC ATAGCAGACT GAGGAGG 27